

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 08:47:56 ; Search time 22 Seconds
(without alignments)
339.663 Million cell updates/sec

Title: US-10-010-227-3
Perfect score: 4055
Sequence: 1 MGAESTPQTLVDKVLQAHV.....KAVPVPITNKGKKEPLEW 778

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2473.5	61.0	758	2 T39210	3-isopropylmalate
2	2456.5	60.6	779	2 S64011	3-isopropylmalate
3	2366	58.3	689	2 S26864	3-isopropylmalate
4	2076	51.2	644	2 U00160	3-isopropylmalate
5	1611	39.7	469	2 AH3271	3-isopropylmalate
6	1586	39.1	475	2 C97684	2-isopropylmalate
7	1584	39.1	469	2 AD2909	3-isopropylmalate
8	1562	38.5	479	2 C87273	3-isopropylmalate
9	1548.3	38.2	469	2 G81128	3-isopropylmalate
10	1545.5	38.1	469	2 AB1836	probable 3-isoprop
11	1507.5	37.2	474	2 G83255	3-isopropylmalate
12	1498.5	37.0	474	2 H82564	3-isopropylmalate
13	1479.5	36.5	466	2 H64728	3-isopropylmalate
14	1477.5	36.4	466	2 AD0516	3-isopropylmalate
15	1471	36.3	469	2 F64163	3-isopropylmalate
16	1469.5	36.2	466	2 D90638	hypothetical prote
17	1469.5	36.2	466	2 DB5489	3-isopropylmalate
18	1452	35.8	476	2 AI0065	3-isopropylmalate
19	1425.5	35.2	467	2 H82070	3-isopropylmalate
20	1413	34.8	485	2 T39699	3-isopropylmalate
21	1396	34.4	472	2 H84031	3-isopropylmalate
22	1393.5	34.4	472	2 B69650	3-isopropylmalate
23	1385.5	34.2	476	2 T29083	3-isopropylmalate
24	1385	34.2	473	2 G70853	probable leuc prot
25	1354	33.4	476	2 T45425	3-isopropylmalate
26	1354	33.4	485	2 G87119	3-isopropylmalate
27	1311.5	32.3	470	2 AB1270	3-isopropylmalate
28	1304.5	32.2	464	2 S10171	3-isopropylmalate
29	1283.5	31.7	462	2 AF1694	3-isopropylmalate

30	1282	31.6	456	2 A89998	3-isopropylmalate
31	1279.5	31.6	462	2 AE1323	3-isopropylmalate
32	1181.5	29.1	468	2 S76826	hypothetical prote
33	1172.5	28.9	467	2 AF1983	3-isopropylmalate
34	1141.5	28.2	460	2 S5134	probable 3-isoprop
35	1132.5	27.9	460	2 D86777	hypothetical prote
36	1114	27.5	459	2 D36889	3-isopropylmalate
37	684.5	16.9	422	2 C70381	large subunit of i
38	662.5	16.3	267	2 T39573	probable 3-isoprop
39	641	15.8	431	2 H75354	3-isopropylmalate
40	640.5	15.8	659	2 F70453	aconitase - Aquife
41	637.5	15.7	423	2 B75045	probable 3-isoprop
42	635	15.7	424	2 D64362	aconitase hydratase
43	613	15.1	419	2 D69051	3-isopropylmalate
44	602.5	14.9	420	2 B64425	3-isopropylmalate
45	599	14.8	642	2 H97019	aconitase A (import
46	597.5	14.7	211	2 AB3561	3-isopropylmalate
47	595.5	14.7	417	2 H72362	3-isopropylmalate
48	587.5	14.5	433	2 B69495	aconitase (acn) ho
49	576.5	14.2	422	2 C97280	3-isopropylmalate
50	573.5	14.1	436	2 G69524	aconitase (importe
51	562	13.9	661	2 H84406	3-isopropylmalate
52	560.5	13.8	216	2 F97693	3-isopropylmalate
53	558.5	13.8	201	2 AE2919	3-isopropylmalate
54	558.5	13.8	509	2 T06300	hypothetical prote
55	552	13.6	428	2 A69085	3-isopropylmalate
56	552	13.6	721	2 T38665	probable homoaconi
57	544	13.4	213	2 C81836	probable 3-isoprop
58	542	13.4	212	2 F83255	3-isopropylmalate
59	542	13.4	213	2 B81128	3-isopropylmalate
60	541.5	13.4	418	2 C72384	hypothetical prote
61	532.5	13.1	693	1 S61067	homoaconitate hydr
62	519	12.8	215	2 G82564	3-isopropylmalate
63	513	12.7	202	2 B87273	3-isopropylmalate
64	512	12.6	434	2 D75373	3-isopropylmalate
65	506	12.5	201	2 AC0516	3-isopropylmalate
66	505	12.5	201	2 S07306	3-isopropylmalate
67	498	12.3	200	2 A82071	3-isopropylmalate
68	495	12.2	200	1 G64106	3-isopropylmalate
69	492	12.1	201	2 C90638	isopropylmalate is
70	492	12.1	201	2 C85489	isopropylmalate is
71	491	12.1	201	2 A50585	3-isopropylmalate
72	482.5	11.9	191	2 E36889	probable 3-isoprop
73	482.5	11.9	780	2 T52543	aconitase hydratase
74	475	11.7	788	2 S44831	aconitase hydratase
75	474	11.7	200	2 AH0065	F54H12.1 protein -
76	467	11.5	194	2 G84031	3-isopropylmalate
77	466.5	11.5	199	2 C69650	3-isopropylmalate
78	462.5	11.4	781	2 A35584	aconitase hydratase
79	447.5	11.0	789	2 S57528	aconitase hydratase
80	444.5	11.0	781	2 S65631	aconitase hydratase
81	443.5	10.9	779	2 S57805	aconitase hydratase
82	439.5	10.8	778	2 T38347	aconitase hydratase
83	434.5	10.7	778	2 S50387	aconitase hydratase
84	422	10.4	200	2 H81269	probable 3-isoprop
85	421	10.4	190	2 B89998	3-isopropylmalate
86	417	10.3	416	2 A99419	hypothetical prote
87	394.5	9.7	887	2 T27868	hypothetical prote
88	393	9.7	870	2 E72541	probable aconitase
89	387	9.5	208	2 T39571	3-isoprop
90	386.5	9.5	906	2 G75362	aconitase hydratase
91	386	9.5	137	2 S73885	3-isopropylmalate
92	384.5	9.5	895	2 A13483	aconitase hydratase
93	384.5	9.5	868	2 B83451	aconitase hydratase
94	384	9.5	868	2 B82213	aconitase hydratase
95	384	9.5	907	2 T04820	aconitase hydratase
96	375.5	9.3	193	2 A11333	3-isopropylmalate
97	375	9.2	386	2 T51171	homoaconitase hydr
98	369.5	9.1	903	2 A87704	aconitase hydratase
99	366.5	9.1	193	2 AG1694	3-isopropylmalate
100	366	9.0	898	2 T10101	aconitase hydratase

Query Match. 58.3%; Score 2366; DB 2; Length 689;
Best Local Similarity 68.4%; Pred. No. 1.4e-157;
Matches 472; Conservative 62; Mismatches 133; Indels 24; Gaps 9;

QY 9 QTLVLYQLQAHVHVDKLDGLVLLYIDRHLYHEVTSPOAEGLRNAGKVRPRPCTLATTTD 68
Db 3 RLVLDKQWMDHV-----IDRHLYHEVTSPOAEGLRNAGKVRPRPCTLATIYD 50

QY 69 HNVFTSRKALKDIAFIEKEDSRTOCVTLSENVKPEFGVYGLSPKROGIVHVIPEQG 128
Db 51 HNPFTTRKFKFSITTFIDEADSRTOCVTLSENVKPEFGVYGLSPKROGIVHVIPEQG 110

QY 129 FTLPFTVWCGDSHTSTHGAFCALAFGIGTSEVEHYLATOCLITKRSKNMRLOVDGELAP 188
Db 111 FTLPFTVWCGDSHTSTHGAFCALAFGIGTSEVEHYLATOCLITKRSKNMRLOVDGELAP 170

QY 189 GVSSKDVLYLAIGIIGTGAGTGAVIEFGGSVTRLSLMEARMSCNNSIGGARAAGWAPD 248
Db 171 GVTSKDVLAHVGIGTGAGTGAVIEFGGSVTRLSLMEARMSCNNSIGGARAAGWAPD 230

QY 249 EITFEYLYKGRPLAPKYDSPEMHKATQYWMKNLOSPDGAKYDIDVFIDAKDIDVPTLTWGTSP 308
Db 231 EITFEYLYKGRPLAP--EAGENDKAVQYWKSLKSDPNPAKIDIDVXIASDIAPIITWTGTS 288

QY 309 EDVVPITGVVDEPETFEATEAKKADGRMLQYMGKAGTPEMDIIVDKVPIGSCCTNSRIED 368
Db 289 QDVAPITANVPDPSVSDPARKAMERALEYIGLVNPTLIEVYKIDKAFIGSCCTNSRIED 348

QY 369 LRAAAAVYKGRKKAPNVKASAVVYPSSGLYKTOAEFGGLDKIFEAEPEMEAGSMCLGM 428
Db 349 LRSAAISYKGRKIAWV-YAVVYPSSGLYKROAERGLKVFEDAGDMREAGSMCLGM 407

QY 429 NPDIAPPOERCASSTNRNPEFGQAGGRTHLMSPVWAAAGIYGLKADYKLTIDYKASPH 488
Db 408 NPDOISPEBERCASTNRNPEFGQAGGRTHLMSPVWAAAGIYGLTDYKFSSTPWVPR 467

QY 489 IAAVQKSTVTRKPHYDERI--NDAHEKDIADIPEDNNGPHNTSASVGTSGAGLPKRTIL 546
Db 468 SPPPKFQRI-QPKVDEDAAHKQADQADPVTDCPP--AGSPVVKGAPEV--ASAMPAFTTL 522

QY 547 KGIAPLEKAVNDPTAIIIPKQFLKTIKRTGLGNALFYEMRFN-EDGERSKDPVLYNKBPYR 605
Db 523 KGVAAPELISVNDVTMIIPKQFLKTIKRTGLGSALFYGLGPDATGAKEKDFVUNQAPYR 582

QY 606 KASIIYVCGANFGCCSSREHAPWALNDFGIRSVIAPSFADIFPNNSFKNGMLPIPIKQDA 665
Db 583 SKKIIYVCGPNNGCCSSREHAPWAFNDFGIRCIATSPADIFPNNSCKNGMLPI-ILSQE 641

QY 666 QIEAIAAPRAGKEIEVDLPNOLIKNATGE 695
Db 642 QVDTLAKYATQKAEIEVDLPVHOKIRYPGGE 671

RESULT 4
J00160 3-isopropylmalate dehydratase (EC 4.2.1.33) - Rhizomucor circinnelloides
N:Alternate names: alpha-3-isopropylmalate isomerase
C:Species: Rhizomucor circinnelloides
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 17-Mar-2000
C:Accession: J00160; S26865
R:Ronceiro, M.I.G.; Jeppsen, L.P.; Ströman, P.; van Heeswijk, R.
Gene 84, 335-343, 1989
A:Title: Characterization of a leuA gene and an AHS element from Mucor circinnelloides.
A:Reference number: J00160; MUID:90128278; PMID:2693214
A:Accession: J00160
A:Molecule type: DNA
A:Residues: 1-644 <R0N>
A:Cross-references: GB:M3166; NID:g168366; PIDN:AAA33422.1; PID:g168367
A>Note: The authors translated the codon ATT for residue 119 as Asn
R:Ruturriaga, E.A.; Diaz-Minguez, J.M.; Benito, E.P.; Alvarez, M.I.; Eslava, A.P.
Curr. Genet. 21, 215-223, 1992
A:Title: Heterologous transformation of Mucor circinnelloides with the Phycomyces blakesleii
Reference number: S26864; MUID:92724296; PMID:1563047

A:Accession: S26865
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-644 <ITU>
C:Comment: This enzyme is involved in the biosynthesis of leucine.
C:Genetics:
A:Gene: leuA
C:Superfamily: homoaconitate hydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 51.2%; Score 2076; DB 2; Length 644;
Best Local Similarity 68.8%; Pred. No. 2.6e-137;
Matches 407; Conservative 60; Mismatches 111; Indels 14; Gaps 6;

QY 10 TLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLATTDH 69
DQ 10 TLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLATTDH 69
DQ 51 TLYDKVMDHVDIQEDDGTCLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLATVDH 110
QY 70 NVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVHVGPEQGF 129
DQ 70 NVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVHVGPEQGF 129
DQ 111 NIPPTTKIFKNITTFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVHVGPEQGF 170
QY 130 TLPPTTVCCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 189
DQ 130 TLPPTTVCCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 189
DQ 171 TLPATTVCCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 230
QY 190 VSKDVLVHHAIGTAGGTGAVTFPCGSVIRSLMSARMSCNMSIEGGARAGVAPDE 249
DQ 190 VSKDVLVHHAIGTAGGTGAVTFPCGSVIRSLMSARMSCNMSIEGGARAGVAPDE 249
DQ 231 VTSKDIVLHTIGVITAGGTGCVTFEGCGDTAALSMSARMSCNMSIEGGARAGVAPDE 290
QY 250 ITEPYLKGRLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTWGTSP 309
DQ 250 ITEPYLKGRLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTWGTSP 309
DQ 291 VTEPYLKGRLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTWGTSP 348
QY 310 DVVPIITGVVDPPTFAEAKKADGRMLQYMGKAGTGMEDIPVDKVFISGCTNSRIEDL 369
DQ 310 DVVPIITGVVDPPTFAEAKKADGRMLQYMGKAGTGMEDIPVDKVFISGCTNSRIEDL 369
DQ 349 DVVPIITGVVDPPTFAEAKKADGRMLQYMGKAGTGMEDIPVDKVFISGCTNSRIEDL 408
QY 370 RAAAVVKGKRAAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 429
DQ 370 RAAAVVKGKRAAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 429
DQ 409 RAAAVVKGKRAAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 467
QY 430 PDLAPQERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVRKLTVDYKASPHI 489
DQ 430 PDLAPQERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVRKLTVDYKASPHI 489
DQ 468 PDLAPQERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVRKLTVDYKASPHI 520
QY 490 AAYQKSTVTKPHYDERINODAEKDIADIPEDNNGPHTNTSASVGTSGALPKFTILKGI 549
DQ 490 AAYQKSTVTKPHYDERINODAEKDIADIPEDNNGPHTNTSASVGTSGALPKFTILKGI 549
DQ 521 SEIPGTPKQSPQEVVAEPESEEDV--DSSSVDSAP-VATPPTGDSAGMPKFTILKGY 577
QY 550 AAPLEXANVDTDAIIPKQFLTKTKRTGLGNALFYEMRFN-EDGTEKSDFVLN 600
DQ 550 AAPLEXANVDTDAIIPKQFLTKTKRTGLGNALFYEMRFN-EDGTEKSDFVLN 600
DQ 578 AAPLDISNVDTDIIPKQFLTKTKRTGLGNALFYEMRFN-EDGTEKSDFVLN 629

RESULT 5
AH3271
3-isopropylmalate dehydratase (EC 4.2.1.33) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C:Accession: AH3271
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AB3252; PMID:11756688
A:Accession: AH3271
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-469 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51339.1; PID:gl7982037; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:

A:Gene: BMEI0157
A:Map position: 1
C:Superfamily: aconitate hydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 39.7%; Score 1611; DB 2; Length 469;
Best Local Similarity 66.8%; Pred. No. 5.9e-105;
Matches 316; Conservative 51; Mismatches 98; Indels 8; Gaps 3;

QY 6 STPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLA 65
DQ 6 STPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLA 65
QY 2 SAPRTLYDKVMDHVDIQEDDGTCLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLA 61
DQ 2 SAPRTLYDKVMDHVDIQEDDGTCLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCTLA 61
QY 66 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVHVG 125
DQ 66 TTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVHVG 125
DQ 62 VVDHNVPTS-----PDRINGIQNEESRIQVEALARNADFGVEYYSERDKRQGIHVHVG 116
QY 126 EOGFTLPGMTIVCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 185
DQ 126 EOGFTLPGMTIVCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 185
DQ 117 EOGFTLPGMTIVCGDSHTSTHGAFAFGAGTSEVEHVLATQCLITKRSKNMRTQVDELAPG 176
QY 186 LAPGVSSKDVVLHHAIGTAGGTGAVTFPCGSVIRSLMSARMSCNMSIEGGARAGV 245
DQ 186 LAPGVSSKDVVLHHAIGTAGGTGAVTFPCGSVIRSLMSARMSCNMSIEGGARAGV 245
DQ 177 LPAGVTAKDIVLHHAIGTAGGTGAVTFPCGSVIRSLMSARMSCNMSIEGGARAGV 236
QY 246 APDETTFYLYKGRPLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTW 305
DQ 246 APDETTFYLYKGRPLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTW 305
DQ 237 APDETTFYLYKGRPLAPKDYSPENHKAQYWKVQLSDPGAKYDIDVFDKADIVPTLTW 294
QY 306 TSPEDVPIITGVVDPPTFAEAKKADGRMLQYMGKAGTGMEDIPVDKVFISGCTNSR 365
DQ 306 TSPEDVPIITGVVDPPTFAEAKKADGRMLQYMGKAGTGMEDIPVDKVFISGCTNSR 365
DQ 295 SSPEDVSVTGVVPPNDIADETKRAKRWALDYGLKPGTKITDIAVDRVFGSCTNGR 354
QY 366 IEDLRAAAVVKGRKAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 425
DQ 366 IEDLRAAAVVKGRKAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 425
DQ 355 IEDLRAAAVVKGRKAPVKSAMVPGSLVKTQAELEGDKIPEEAGFWEAGCSMCLGMN 413
QY 426 LGMPDILAPQERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVR 478
DQ 426 LGMPDILAPQERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVR 478
DQ 414 LAMNDRLLKPGERCASTSNRNFEGRGAGGRTGLMSPVMAAAGIVGKLADVR 466

RESULT 6
C97684
2-isopropylmalate isomerase large chain (AJ236268) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: C97684
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorillo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A:Reference number: A97359; PMID:11743194
A:Accession: C97684
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88428.1; PID:gl5157923; GSPDB:GN00169
C:Genetics:
A:Gene: AGR C 4910
A:Map position: circular chromosome
C:Superfamily: aconitate hydratase

Query Match 39.1%; Score 1586; DB 2; Length 475;
Best Local Similarity 65.3%; Pred. No. 3.4e-103;
Matches 311; Conservative 52; Mismatches 105; Indels 8; Gaps 3;

QY 4 AESTPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCT 63
DQ 4 AESTPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCT 63
DQ 6 AMSAPRTLYDKVMDHVDIQEDDGTCLYIDRHLVHEVTSPOAFEGRLNAGRKVRRPDCT 65
QY 64 LATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVH 123
DQ 64 LATTDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFGVTFGLSDKQGIHVH 123

Db 66 LAVVDHNVPTTA-----DRLEGIKNESRIQVEALAQNAKERGVYERDKQGIYVHT 120

Qy 124 GPRGGFTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 183

Db 121 GPRGGFTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 180

Qy 184 GELAPGVSSKDVVLAIGITAGTGAIVIEFCGIVTSLSMSEARMSICNMSIEGGARAG 243

Db 181 GKLPESYTAQDIIIAIIGELGTAGTGIVIEFAGAIRSLSMSEGMTVCNMITEGGARAG 240

Qy 244 MVNPDELTFEYLKGRPLAPKYDSPEMHKATQYWKULQSPGKAYDIDVFDKDIPTLT 303

Db 241 LIAPDELTFDITKGRPRAPKGETLE--QAIYWKTLKSDGHAHYTKVILLDAANLPPIVS 298

Qy 304 WGTSPEDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTN 363

Db 299 WGTSPEDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTN 358

Qy 364 SRLEDLRAAAAVVKGKKAQVNVKAMVYVPGSLVKTQAEBSGLDKIFEEAGFEWREAGCS 423

Db 359 GRLEDLRAAAKIVDKGRKVAATV-SAMIVPGSGLVKEQAEKEGLDKIFLDAGFEWREPGCS 417

Qy 424 MCGMNPDIILAPORCASTSNRNFEGROGAGGRTHLMSPVMAAAAGIVGKLADVRK 479

Db 418 MCLAMNDRLKPERCASTSNRNFEGROGYKSRTHLVSPAMAAAAIAGHFVDVRE 473

RESULT 7

3-isopropylmalate dehydratase, large subunit [imported] - Agrobacterium tumefaciens (str AD2909

C/Species: Agrobacterium tumefaciens

C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C/Accession: AD2909

R/Wood, D.W.; Secubai, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Kreespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.

A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A/Reference number: AB2577; PMID:11743193

A/Accession: AD2909

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-469 <KOR>

A/Cross-references: GB:AE008688; PIDN:AA143690.1; PID:gl7741217; GSPDB:GN00186

A/Experimental source: strain C58 (Dupont)

C/Genetics:

A/Gene: leuc

A/Map position: circular chromosome

C/Superfamily: aconitate hydratase

Query Match 39.1%; Score 1584; DB 2; Length 469;

Best Local Similarity 65.4%; Pred. No. 4.6e-103;

Matches 310; Conservative 52; Mismatches 104; Indels 8; Gaps 3;

Qy 6 STPGTLYDQVLAHVVDKLGSTVLLYIDRHLVHEVTSPOAFEGELNARKVRPDDCTLA 65

Db 2 SAPRTLYDKIMDDHVNADPDGTCILYIDRHLVHEVTSPOAFEGELNARKVRPDDCTLA 61

Qy 66 TTDHNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHIGP 125

Db 62 VVDHNVPTTA-----DRLEGIKNESRIQVEALAQNAKEFGVYERDKQGIYVHIGP 116

Qy 126 EOGTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 185

Db 117 EOGTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 176

Qy 186 LAPGVSSKDVVLAIGITAGTGAIVIEFCGIVTSLSMSEARMSICNMSIEGGARAG 245

Db 177 LPESYTAQDIIIAIIGELGTAGTGIVIEFAGAIRSLSMSEGMTVCNMITEGGARAG 236

Qy 246 APDELTFEYLKGRPLAPKYDSPEMHKATQYWKULQSPGKAYDIDVFDKDIPTLT 305

Db 237 APDELTFDITKGRPRAPKGETLE--QAIYWKTLKSDGHAHYTKVILLDAANLPPIVS 294

Qy 306 TSPEDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSR 365

Db 295 TSPEDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSR 354

Qy 366 IEDLRAAAAVVKGKKAQVNVKAMVYVPGSLVKTQAEBSGLDKIFEEAGFEWREAGCS 425

Db 355 IEDLRAAAKIVDKGRKVAATV-SAMIVPGSGLVKEQAEKEGLDKIFLDAGFEWREPGCS 413

Qy 426 ICGMNPDIILAPORCASTSNRNFEGROGAGGRTHLMSPVMAAAAGIVGKLADVRK 479

Db 414 LAMNDRLKPERCASTSNRNFEGROGYKSRTHLVSPAMAAAAIAGHFVDVRE 467

RESULT 8

3-isopropylmalate dehydratase, large subunit [imported] - Caulobacter crescentus C87273

C/Species: Caulobacter crescentus

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C/Accession: C87273

R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolm n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A/Title: Complete Genome Sequence of Caulobacter crescentus.

A/Reference number: A87249; PMID:11173698; PMID:11259647

A/Accession: C87273

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-479 <STO>

A/Cross-references: GB:AE005673; NID:G13421319; PIDN:AAK2183.1; GSPDB:GN00148

C/Genetics:

A/Gene: CC0196

C/Superfamily: aconitate hydratase

Query Match 38.5%; Score 1562; DB 2; Length 479;

Best Local Similarity 64.4%; Pred. No. 1.6e-101;

Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;

Qy 9 QTIYDKTLQAHVVDKLGSTVLLYIDRHLVHEVTSPOAFEGELNARKVRPDDCTLATTD 68

Db 4 KTIYDKTIMDAHVSE--AGGAILYIDHLVHEVTPQAFGLRAAGRKVRPDDCTLATVD 62

Qy 69 HNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHIGP 128

Db 63 HNVPTTSRKALKDIAFIKEDDSRTQCVTLSENVKEFGVTYFGLSDRKQGIYVHIGP 119

Qy 129 FTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 188

Db 120 FTLPSTTVVCGDSHTSTHGAFGALAFGISTSEVENHLATQCLITKRSKNMRIOVD 179

Qy 189 GVSCKDVVLAIGITAGTGAIVIEFCGIVTSLSMSEARMSICNMSIEGGARAG 248

Db 180 GVSCKDVVLAIGITAGTGAIVIEFCGIVTSLSMSEARMSICNMSIEGGARAG 239

Qy 249 EITFEYLKGRPLAPKYDSPEMHKATQYWKULQSPGKAYDIDVFDKDIPTLT 308

Db 240 EITFEYLKGRPLAPKYDSPEMHKATQYWKULQSPGKAYDIDVFDKDIPTLT 297

Qy 309 EDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSRIED 368

Db 298 EDVVPITGVPPDETFATEAKKADGRMLQYMGKAGTPMEDIPVDKVFISGCTNSRIED 357

Qy 369 LRAAAAVVKGKKAQVNVKAMVYVPGSLVKTQAEBSGLDKIFEEAGFEWREAGCS 423

Db 358 LRAAAAVVKGKKAQVNVKAMVYVPGSLVKTQAEBSGLDKIFEEAGFEWREAGCS 416

Qy 424 MCGMNPDIILAPORCASTSNRNFEGROGAGGRTHLMSPVMAAAAGIVGKLADVRK 480

Db 417 MCLAMNDRLKPERCASTSNRNFEGROGYKSRTHLVSPAMAAAAIAGHFVDVRE 473

RESULT 9

G81128
3-isopropylmalate dehydratase, large chain NMB1036 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81128
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Valleron, A.J. Nature 404, 502-506, 2000
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; PMID:20175755; PMID:10710307
A:Accession: G81128
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-469 <TET>
A:Cross-references: GB:AE002098; GB:AE002454; GB:AE002098; NID:G7226273; PIDN:AAF41435.1; PID:G7226273
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1036
C:Superfamily: aconitate hydratase

Query Match 38.2%; Score 1548.5; DB 2; Length 469;
Best Local Similarity 63.6%; Pred. No. 1.4e-100;
Matches 302; Conservative 62; Mismatches 102; Indels 9; Gaps 3;

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QY 7 TPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAPEGRLNAGRKVRPDCITLAT 66
DB 2 TAQTLYDKLWNSHVREEDGTLLYIDRHLVHEVTSPOAPEGRLNAGRKLRIDSIVVST 61

QY 67 TDHNVPTTSRKALKDIASFTKEDDSRTQCVTLEENVKEFG-VTYFGLSKRQGIHVHVG 125
DB 62 ADHNTPT-----GDWDKGIQDPISKLVDTLDKNIKEFGALAYFPFMDKQGIHVHVG 115

QY 126 EQGFTLPGTTCVCGDSHTSTHGAFGALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGE 185
DB 116 EQGATLPGMTVVCDSHTSTHGAFGALAHGIGTSEVHTMATQCTITAKSKSMLIAVDGK 175

QY 186 LAPGVSSKDVVLHAIGITAGGTGAVIEFCGVSIVRSLSMEARMSICNMSTEGGARAGMV 245
DB 176 LKAGVTAKDVALYIIIGIQTAGGTGVAIEFGGEAIRSLSMGRMTLCNMAIEAGARSGMV 235

QY 246 APDEITFEYLKGRPLAPKYDSPWHKATQYKNLQSDPGAKYDIDVIDAKDIVPTLTWG 305
DB 236 AVDQTTIDYVKDKPFAPEGEA--WDKAVEYWRITLVSDEGAVDFKEYRFAEDIEPQVTWG 293

QY 306 TSPEDVVPITGVVDPPETFATEAKKADGRMLQVMGLKAGTPEMEDIPTDKVFIGSCTNSR 365
DB 294 TSPVMDLISCKVPNPAEETDPVKRSGMERALEYMGLEAGTPEINIPVDIVFIGSCTNSR 353

QY 366 IEDLRAAAAVVKRKAPNVKSAMVPGSLVKTQAEEGDLKIFEEAGFEWREAGSCMC 425
DB 354 IEDLRAAAIAKDKRAANVQVRLVPGSLVKEQAEKGLDKIFIEAGFEWREPGSCMC 413

QY 426 LGMNPDLAPOERCASSTNRNPFEGQAGGRTHLMSVMAAAAGIVGLADVRKL 480
DB 414 LAMNADRLTPGQRCASSTNRNPFEGQNGGRTHLVSPMAAAAATVGRFTDIRMM 468
```

RESULT 10

A81836
probable 3-isopropylmalate dehydratase (EC 4.2.1.33) large chain NMA1450 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81836
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A.; Barlow, J.; White, O.; Rutherford, K.; Staden, R.; Paulsen, O. Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. A:Reference number: A81775; PMID:20222556; PMID:10761919
A:Accession: A81836

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-469 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:G7380091; PIDN:CAB84686.1; PID:G7380091
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: leuC; NMA1450
C:Superfamily: aconitate hydratase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 38.1%; Score 1545.5; DB 2; Length 469;
Best Local Similarity 63.4%; Pred. No. 2.3e-100;
Matches 301; Conservative 62; Mismatches 103; Indels 9; Gaps 3;

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QY 7 TPQTLYDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAPEGRLNAGRKVRPDCITLAT 66
DB 2 TAQTLYDKLWNSHVREEDGTLLYIDRHLVHEVTSPOAPEGRLNAGRKLRIDSIVVST 61

QY 67 TDHNVPTTSRKALKDIASFIKEDDSRTQCVTLEENVKEFG-VTYFGLSKRQGIHVHVG 125
DB 62 ADHNTPT-----GDWDKGIQDPISKLVDTLDKNIKEFGALAYFPFMDKQGIHVHVG 115

QY 126 EQGFTLPGTTCVCGDSHTSTHGAFGALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGE 185
DB 116 EQGATLPGMTVVCDSHTSTHGAFGALAHGIGTSEVHTMATQCTITAKSKSMLIAVDGK 175

QY 186 LAPGVSSKDVVLHAIGITAGGTGAVIEFCGVSIVRSLSMEARMSICNMSTEGGARAGMV 245
DB 176 LKAGVTAKDVALYIIIGIQTAGGTGVAIEFGGEAIRSLSMGRMTLCNMAIEAGARSGMV 235

QY 246 APDEITFEYLKGRPLAPKYDSPWHKATQYKNLQSDPGAKYDIDVIDAKDIVPTLTWG 305
DB 236 AVDQTTIDYVKDKPFAPEGEA--WDKAVEYWRITLVSDEGAVDFKEYRFAEDIEPQVTWG 293

QY 306 TSPEDVVPITGVVDPPETFATEAKKADGRMLQVMGLKAGTPEMEDIPTDKVFIGSCTNSR 365
DB 294 TSPVMDLISCKVPNPAEETDPVKRSGMERALEYMGLEAGTPEINIPVDIVFIGSCTNSR 353

QY 366 IEDLRAAAAVVKRKAPNVKSAMVPGSLVKTQAEEGDLKIFEEAGFEWREAGSCMC 425
DB 354 VEDLRAAAIAKDKRAANVQVRLVPGSLVKEQAEKGLDKIFIEAGFEWREPGSCMC 413

QY 426 LGMNPDLAPOERCASSTNRNPFEGQAGGRTHLMSVMAAAAGIVGLADVRKL 480
DB 414 LAMNADRLTPGQRCASSTNRNPFEGQNGGRTHLVSPMAAAAATVGRFTDIRMM 468
```

RESULT 11

G83255
3-isopropylmalate dehydratase large subunit PA3121 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83255
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adamson, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen. A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: G83255
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-474 <STO>
A:Cross-references: GB:AE004736; GB:AE004091; NID:G9949227; PIDN:AAG06509.1; GSPDB:G06509.1
A:Experimental source: strain PA01
C:Genetics:
A:Gene: leuC; PA3121
C:Superfamily: aconitate hydratase

Query Match 37.2%; Score 1507.5; DB 2; Length 474;
Best Local Similarity 62.5%; Pred. No. 1.1e-97;
Matches 295; Conservative 61; Mismatches 113; Indels 3; Gaps 2;

A;Cross-references: EMBL:D17631; NID:g409068; PID:g2160235

A;Experimental source: strain K-12

C;Genetics:

A;Gene: leuC

C;Function:

A;Pathway: leucine biosynthesis

C;Superfamily: aconitate hydratase

C;Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine biosynthesis

F;347,407,410/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 36.5%; Score 1479.5; DB 2; Length 466;

Best Local Similarity 62.1%; Pred. No. 9.5e-96;

Matches 293; Conservative 59; Mismatches 111; Indels 9; Gaps 4;

QY 9 QTLYDKVLQAHVVDKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPPDCTLATTD 68

DB 3 KTLYEKLFDAHVVEAEENETPLLYIDRHLVHEVTSPOAFDGLRAHGRVPQPKTFTATMD 62

QY 69 HNVPTTSRKALKDIASTFKEDDSRTQCVTLEENVKFVGTVYFGLSDKRGQIVHVGPEQG 128

DB 63 HNVSTQT---KDINAC--GEMARIQMOELIKNCKEFGVELYDLNHPYQGIHVHVGPEQG 116

QY 129 FTLPGTIVVCGDSHTSHGAFALFGIGTSEVHVLATQCLITKRSKNMRLQVGDGLAP 188

DB 117 VTLPGMTIVCGDSHTATHGAFALFGIGTSEVHVLATQCLITKRAKTMKIEVTGNAAP 176

QY 189 GVSSKDVVLHAIGTIGTAGTGAVIEFCGVSIRLSMEARMSICNMSTEGGARAGMVAPD 248

DB 177 GITAKDIVLAIIKGTSGAGTGHHVVEFCGEAIRDLSEGRMTLCNMAIENGAKAGLVAPD 236

QY 249 EITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVIDAKDIIPTLTWTGTS 308

DB 237 ETTFNYYKGRHLHAPK--GKDFDAVAYWKTQTDEGATFTVVTQLQAEIISPQVWTG 294

QY 309 EDVVPITGVVDPDETATEAKKADGRMLQYMGKAGTPEMEDIPTVDKVFISGCTNSRIED 368

DB 295 QGVISVNDNIIDPASADPVERASAEKALAYMGLQPGIPLTEVAIDKVFISGCTNSRIED 354

QY 369 LRAAAAVVKGKAPNVKSAVVPGSGLVKTQAEIEGLDKIFEEAGFEWREAGCSMCLGM 428

DB 355 LRAAAEIAKGRKVPAGVQ--ALVVPGSPVKAQAEAGLDKIFIEAGFEWRLPGCSMCLAM 413

QY 429 NPDILAPQERCASTSNRNPFGRQAGGRTHLMSPVMAAAAGIVGKLADVRKL 480

DB 414 NNDRLNPGERCASTSNRNPFGRQGRGRTHLVSPAMAAAAAATGHFADIRNI 465

RESULT 14

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: EMBL:D17631; NID:g409068; PID:g2160235

A;Experimental source: strain K-12

C;Genetics:

A;Gene: leuC

C;Function:

A;Pathway: leucine biosynthesis

C;Superfamily: aconitate hydratase

C;Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine biosynthesis

F;347,407,410/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 36.5%; Score 1479.5; DB 2; Length 466;

Best Local Similarity 62.1%; Pred. No. 9.5e-96;

Matches 293; Conservative 59; Mismatches 111; Indels 9; Gaps 4;

QY 9 QTLYDKVLQAHVVDKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPPDCTLATTD 68

DB 3 KTLYEKLFDAHVVEAEENETPLLYIDRHLVHEVTSPOAFDGLRAHGRVPQPKTFTATMD 62

QY 69 HNVPTTSRKALKDIASTFKEDDSRTQCVTLEENVKFVGTVYFGLSDKRGQIVHVGPEQG 128

DB 63 HNVSTQT---KDINAC--GEMARIQMOELIKNCKEFGVELYDLNHPYQGIHVHVGPEQG 116

QY 129 FTLPGTIVVCGDSHTSHGAFALFGIGTSEVHVLATQCLITKRSKNMRLQVGDGLAP 188

DB 117 VTLPGMTIVCGDSHTATHGAFALFGIGTSEVHVLATQCLITKRAKTMKIEVTGNAAP 176

QY 189 GVSSKDVVLHAIGTIGTAGTGAVIEFCGVSIRLSMEARMSICNMSTEGGARAGMVAPD 248

DB 177 GITAKDIVLAIIKGTSGAGTGHHVVEFCGEAIRDLSEGRMTLCNMAIENGAKAGLVAPD 236

QY 249 EITFEYLKGRPLAPKYDSPWHKATQYWKNLQSDPGAKYDIDVIDAKDIIPTLTWTGTS 308

DB 237 ETTFNYYKGRHLHAPK--GKDFDAVAYWKTQTDEGATFTVVTQLQAEIISPQVWTG 294

QY 309 EDVVPITGVVDPDETATEAKKADGRMLQYMGKAGTPEMEDIPTVDKVFISGCTNSRIED 368

DB 295 QGVISVNDNIIDPASADPVERASAEKALAYMGLQPGIPLTEVAIDKVFISGCTNSRIED 354

QY 369 LRAAAAVVKGKAPNVKSAVVPGSGLVKTQAEIEGLDKIFEEAGFEWREAGCSMCLGM 428

DB 355 LRAAAEIAKGRKVPAGVQ--ALVVPGSPVKAQAEAGLDKIFIEAGFEWRLPGCSMCLAM 413

QY 429 NPDILAPQERCASTSNRNPFGRQAGGRTHLMSPVMAAAAGIVGKLADVRKL 480

DB 414 NNDRLNPGERCASTSNRNPFGRQGRGRTHLVSPAMAAAAAATGHFADIRNI 465

RESULT 14

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-469 <TIGR>

A;Cross-references: GB:U327779; GB:L42023; NID:g1574009; PID:AAC22649.1; PID:g1574017

A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Accession: F64163

A;Reference number: A64000; MUID:95350630; PMID:7542800

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: A10085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-476 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89388.1; PID:g15978624; GSPDB:GN00175
C;Genetics:
C;Superfamily: aconitate hydratase
A;Gene: leuc
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 35.8%; Score 1452; DB 2; Length 476;
Best Local Similarity 59.2%; Pred. No. 8.2e-94;
Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;

Qy 1 MPGAESTPOTLYDKVLQAHVDEKLDGTULLYIDRHLVHEVTSPOAFEGRLNAGRKVRP 60
Db 1 MGTSSQSKTLQYKLYDAHIVHEAPNETPLLYIDRHLVHEVTSPOAFDGLRAGRPVRQP 60
Qy 61 DCLATTDHNVPTTSRKALKDIASFIEDDSRTQCVTLLENVKEFGVTFGLSDKRGIV 120
Db 61 GKTFTATMDHNVSTQT----KDINA--SGEWARIQMQLINKCAEFGLVSLYDLNHPFGIV 114
Qy 121 HVIGPQGTPLPOTTVVCGDSHTSTHGAFGALAFGIGTSEVHVLAATQCLITKRSKNMRI 180
Db 115 HVIGPQGTPLPOTTVVCGDSHTATHGAFGSLAFGIGTSEVHVLAATQCLITKQRAKTMRI 174
Qy 181 QVDGELAPGVSSKDVVLHAIGITAGGTGAVTEFCGVSIRSLMEARMSICNMSIEGGA 240
Db 175 EVNGTVGAGITAKDVLAIIGTGSAGTGHHVVEFCGSAEALSMGRTLCNNIAENGA 234
Qy 241 RAGMVAPEITFPYLRPLAPKYDSEVHKATQYWKNLQSDPGAKYDIDVFDIAKDIVP 300
Db 235 KAGLVAPDPTTFAYLKGKQFAP--TGQWEGGVAVYWTLSADADAQFDITVTLDAADIAP 292
Qy 301 TLTWGTSPEVVPITGVVPPDPTFATEAKKADGRMLQYMKLGKAGTWMEDIPVDKVFIS 360
Db 293 QVTWGTNPGQVIAVNIIPAESFSDPVERASAEKALAYMDLRFGIKLTEVAIDKVFIS 352
Qy 361 CTNSRIEDLRAAAAVKRGKAPNVKSAMVPGSLVKTQAEELGDKIPFEAGFEWREA 420
Db 353 CTNSRIEDLRAAAVIAQGRKVAQGVQ-AIVVPGSGPVKAQAEGLDKIFIAAGFEWELP 411
Qy 421 GCSMCLGMNPDILAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVGKLADVKRL 480
Db 412 GCSMCLAMNDRLEPGERCASTSNRNFEGRQGRGTHLVSPMAAATAAGHFEVDREL 471
Qy 481 TDYKASPH 488
Db 472 S---ATTH 476

RESULT 19
H82070
3-isopropylmalate dehydratase, large chain VC2492 [similarity] - Vibrio cholerae (strain
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: H82070
R;Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charldson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, B
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82070
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-467 <HEI>

A;Cross-references: GB:AE004318; GB:AE003852; NID:g9657063; PIDN:AAF95634.1; GSPDB:G
A;Experimental source: serogroup O1; strain N16961; biotype E1 for
C;Genetics:
A;Gene: VC2492
A;Map position: 1
C;Superfamily: aconitate hydratase

Query Match 35.2%; Score 1425.5; DB 2; Length 467;
Best Local Similarity 58.9%; Pred. No. 5.7e-92;
Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;

Qy 6 STQOTLYDKVLQAHVDEKLDGTULLYIDRHLVHEVTSPOAFEGRLNAGRKVRPDCDTLA 65
Db 2 SKATLYEKIYDAHVVAAPGETPILYIDRHLVHEVTSPOAFDGLRAGRPVRQVSKTFA 61
Qy 66 TTDHNVPTTSRKALKDIASFIEDDSRTQCVTLLENVKEFGVTFGLSDKRGIVVHVIGP 125
Db 62 TMDHNVSTTT----KDINA--SGEWARIQMQLINKCNEEFVTLVDINHXYQGIHVHVMGP 115
Qy 126 EQGFTLPGTTTVVCGDSHTSTHGAFGALAFGIGTSEVHVLAATQCLITKRSKNMRIQVDGE 185
Db 116 ELGTTLPGMTIVCGDSHTATHGAFGSLAFGIGTSEVHVLAATQCLITKQRAKTMKIEVRGK 175
Qy 186 LAPGVSSKDVVLHAIGITAGGTGAVTEFCGVSIRSLMEARMSICNMSIEGGRAGMV 245
Db 176 VAPGITAKDVLAIIGTGAAGGTGVVVEFCGEAIRDLSEGRMTVCNMAIELGAKAGLI 235
Qy 246 APDITTEYLKGRPLAPKYDSEVHKATQYWKNLQSDFGAKYDIDVFDIAKDIVPFLTWG 305
Db 236 APDATTFNVIKGRFAPQ--GSDWDAVDYMQTLTKLDEDAQFDVAVTLEASEIKPQVTWG 293
Qy 306 TSPEDVVPITGVVPPDPTFATEAKKADGRMLQYMKLGKAGTWMEDIPVDKVFISCTNSR 365
Db 294 TNPQGVIAVDEPIPSQSFADPVERSAEKALAYMGLSEAGKMLSDYKVDKVFVGSCTNSR 353
Qy 366 IEDLRAAAAVKRGKAPNVKSAMVPGSLVKTQAEELGDKIPFEAGFEWREAGCSMC 425
Db 354 IEDMRAAAAVKRGKAVSHVQ-ALIVPQSEVKAQAEGLDKIFIEAGFEWRLPGCSMC 412
Qy 426 LGMPDIIAPQERCASTSNRNFEGRQAGGRTHLMSPVMAAAGIVGKLADVKR 479
Db 413 LAMNDRLPGERCASTSNRNFEGRQGRGTHLVSPMAAATAAGHFEVDIRQ 466

RESULT 20
I39699
3-isopropylmalate dehydratase (EC 4.2.1.33) large chain - Actinoplanes teichomycetic
N;Alternate names: isopropylmalate isomerase large chain
C;Species: Actinoplanes teichomyceticus
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 24-Nov-1999
C;Accession: I39699
R;Castelli, P.; Donadio, S.; Marinelli, F.; Borghi, A.; Sosio, M.
Gene 158, 97-100, 1995
A;Title: Complementatation of a Streptomyces lividans Leu- mutant by the Actinoplanes
A;Reference number: I39699; MUID:95309734; PMID:7789819
A;Accession: I39699
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-485 <RES>
A;Cross-references: EMBL:X84647; NID:g1008941; PIDN:CAA59140.1; PID:g1008942
A;Experimental source: ATCC 31121
C;Genetics:
A;Gene: leuc
C;Function:
A;Pathway: leucine biosynthesis
C;Superfamily: aconitate hydratase
C;Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine
F;367,427,430/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 34.8%; Score 1413; DB 2; Length 485;
Best Local Similarity 59.7%; Pred. No. 4.6e-91;
Matches 285; Conservative 51; Mismatches 125; Indels 16; Gaps 5;

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QY      8 PQTLYDKVLAHVHVDKLDGTV-LIYIDRHLVHEVTSPOAFEGRLNAGRKVRPPDCTLAT 66
      11 PRTIAEKWWDHVVRTAAEGEBDLIFIDHLHHEVTSPOAFDGLRMAGRVVRTDILTAT 70
QY      67 TDHNVPT-----TSKALKDIASFIKEDDSRTQCVTLEENVKEFGVTYFELSRRQG 118
      71 EDHNTPTGYADPSEFNRKRGELTTLADTV---SRQIETLRKNCAEFGEYIRPLGQVNGG 126
QY      119 IVHVIQEGQFTLPGTVVCGDSHTSTHGAFGALAFIGTSEVENHVALTOCLITRKSXNM 178
      127 IVHVIQPLGLTQCGMTIVCGDSHTATGASALAFIGTSEVENHVALTOCLITRKSXNM 186
QY      179 RIQVDBELAPVSSKDVVLAIGITGAGTGAVIDFCGVSIRLSMEARMSICNMSIEG 238
      187 AVTVVGEIRPVSAAKDLITLITGTGTGGNGHIVEYRGEAIRKLSMEGRMTICNMSIEM 246
QY      239 GARAGMVAPEDEITEEYLKGRPLAPKYDSEPMHKAQYVMGNLOSDDGAKKDIVDFIDAKI 298
      247 GAKAGMVAPEDEITEEYLKGRPLAPKYDSEPMHKAQYVMGNLOSDDGAKKDIVDFIDAKI 304
QY      299 VPTLTWGTSPEDVVPITGVDPPEFATEAKKADGRMLQYMGKLAGTPEMEDIIVDKVFI 358
      305 SPFTTWGTNPGQALDGVDPDQDFLDEVERGAERALAVMGLTPTGTFRDVDPVDVFEV 364
QY      359 GSCCTNSRIEDIRAAAVKGRKKADPNVKSAMVPGSGLVKTQAEERGLDKIFEAGFEWR 418
      365 GSCCTNGRLIEDIRAAADVIRGRKKVADGVV-MMIVPGSYVREQAERGLDKIFIDAGAEWR 423
QY      419 EAGSMCLGNMPTLAPQERCASTSNRNFEGRQAGRTHLMSPVMAAAGIVGKLA 475
      424 FAGSMCLGNMPTLSPQRAASTSNRNFEGRQAGRTHLMSPVMAAATAVVAGKLA 480
Db
RESULT 21
H84031
3-Isopropylmalate dehydratase large subunit leuc (imported) - Bacillus halodurans (strat
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84031
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H84031
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <STO>
A:Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA06775.1; GSPDB:GN0
A:Experimental source: strain C-125
C:Genetics:
C:Superfamily: aconitate hydratase
Query Match      34.4%; Score 1396; DB 2; Length 472;
Best Local Similarity 59.28; Pred. No. 6.8e-90;
Matches 279; Conservative 58; Mismatches 124; Indels 10; Gaps 3;
QY      8 PQTLYDKVLAHVHVDKLDGTVLIYIDRHLVHEVTSPOAFEGRLNAGRKVRPPDCTLAT 67
      11 PRTIAEKWWDHVVRTAAEGEBDLIFIDHLHHEVTSPOAFDGLRMAGRVVRTDILTAT 70
QY      3 PRTIETKIMDAHYVIGEGKPSLYIDHMHVETSPQAFEGRLNAGRPVRPDLPTATM 62
      68 DHNVPTTSRKALDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDRKQGIHVHIGEQ 127
      63 DHNVPTVDRFNIOD-----QIARKQIETLEANCKEFGIEIAGDSPNNGIVHIGPEL 115
QY      128 GFTLPGTVVCGDSHTSTHGAFGALAFIGTSEVENHVALTOCLITRKSXNMRIQVDBELA 187
      116 GLTQPGKTVVCGDSHTSTHGAFGALAFIGTSEVENHVALTOCLITRKSXNMRIQVDBELA 175
QY      188 PGVSSKDVVLAHIGITGAGTGAVIDFCGVSIRLSMEARMSICNMSIEGARAQVAP 247
      176 PVSASADIIILAVIAKGVDPGTGVIERTGSAIRLSMEARMTICNMSIEGAKAGLISP 235
Db

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QY      248 DEITFEYLKGRPLAPKYDSEPMHKAQYVMGNLOSDDGAKKDIVDFIDAKDIVPTLTWGT 307
      236 DSATFEYLKGRPLAPKYDSEPMHKAQYVMGNLOSDDGAKKDIVDFIDAKDIVPTLTWGT 293
Db
QY      308 PEDVPTGVDPPEFATEAKKADGRMLQYMGKLAGTPEMEDIIVDKVFIQSCCTNSRIE 367
      294 PAQGTGQVVPSPDDKADENERRAIRKQSLAVMGLTPTGTFRDVDPVDVFEV 353
QY      368 DLAAAAVAVKGRKKADPNVKSAMVPGSGLVKTQAEERGLDKIFEAGFEWR 427
      354 DLRTAEHLIRGRKVDVIR-ALVVPSSQVYRAEKGLDIFFEAGFEWRDSCSMCLG 412
Db
QY      428 MNPDIAPQERCASTSNRNFEGRQAGRTHLMSPVMAAAGIVGKLA 478
      413 MNPDIAPQERCASTSNRNFEGRQAGRTHLMSPVMAAAGIVGKLA 463
Db
RESULT 22
B69650
3-Isopropylmalate dehydratase (EC 4.2.1.33) large chain - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: B69650
R:Kunze, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertec
C.; Bron, S.; Brouillette, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Filtz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
koeth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.;
Kletter, P.; Koningsstein, G.; Krogh, S.; Kurita, K.; Lapidos, A.; Lardinois,
A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Yata, K.; Yoshida, K.
Y, M.; Ogawa, K.; Ogiwara, A.; Oudeg, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,
A.; Authors: Tanakoshi, A.; Tanaka, T.; Tepstein, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Whitters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69650
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-472 <KUN>
A:Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CA014786.1; PID:g2635291
A:Experimental source: strain 168
C:Genetics:
A:Gene: leuc
A:Function:
A:Pathway: leucine biosynthesis
C:Superfamily: aconitate hydratase
C:Keywords: 4Fe-4S; carbon-oxygen lyase; hydro-lyase; iron-sulfur protein; leucine biosy
F.347,407,410/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
Query Match      34.4%; Score 1393.5; DB 2; Length 472;
Best Local Similarity 56.5%; Pred. No. 1e-89;
Matches 277; Conservative 63; Mismatches 129; Indels 21; Gaps 4;
QY      8 PQTLYDKVLAHVHVDKLDGTVLIYIDRHLVHEVTSPOAFEGRLNAGRKVRPPDCTLAT 67
      11 PRTIAEKWWDHVVRTAAEGEBDLIFIDHLHHEVTSPOAFDGLRMAGRVVRTDILTAT 70
QY      3 PRTIETKIMDAHYVIGEGKPSLYIDHMHVETSPQAFEGRLNAGRPVRPDLPTATM 62
      68 DHNVPTTSRKALDIASFIKEDDSRTQCVTLEENVKEFGVTYFGLSDRKQGIHVHIGEQ 127
      63 DHNVPTVDRFNIOD-----EYARKQVYALFNCEBFGRLADHSDVDGIVHVGPEL 115
QY      128 GFTLPGTVVCGDSHTSTHGAFGALAFIGTSEVENHVALTOCLITRKSXNMRIQVDBELA 187
      116 GLTQPGKTVVCGDSHTSTHGAFGALAFIGTSEVENHVALTOCLITRKSXNMRIQVDBELA 175
QY      188 PGVSSKDVVLAHIGITGAGTGAVIDFCGVSIRLSMEARMSICNMSIEGARAQVAP 247
      176 KQVTAQDVILAVIAGYKGVGTGVIERTGSAIRLSMEARMTICNMSIEGAKAGLISP 235
Db

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A:Reference number: Z16918
A:Accession: T45425
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-476 <PAR>
A:Cross-References: EMBL:Z99263, PIDN:CAB16447.1
A:Experimental source: cosmid B637
C:Genetics:
A:Note: leuc
C:Superfamily: aconitase hydratase

Query Match 33.4%; Score 1354; DB 2; Length 476;
Best Local Similarity 56.9%; Pred. No. 6e-87;
Matches 272; Conservative 55; Mismatches 131; Indels 20; Gaps 5;

QY 3 GAESTPQTLVDKYLQAHV-----DEKLDGTVLLYIDRHLYHEVTSPOAFEGELRNAG 54
DB 2 GGARKPRTLAEKWDDHVVAGQGYHODR--GPDLYIDHLYHEVTSPOAFDGLRLAG 58
QY 55 RKYRRPDCTLATTDHNVPTTSRKALKDIAEFKEDSDRTQCVTLEENVKEFGVTFGLSD 114
DB 59 RMYRRPDLTVATBDHNVPTV-----DIDKPIADPVSRIGVETLRRNCAEFGVRLHPMGD 112
QY 115 KRQGIYHVIPEQGFILPGTTVCGDSHTSTHGAFGALARGIGTSEVHVLTATQCLITKR 174
DB 113 IEOGIYHVVGPQLGTQPGMTIVCGDSHTSTHGAFGAIAIMGIGTSEIEHVLATQTLPLRP 172
QY 175 SKRMRIQVDELAPGVSSKVVVLAIGITAGGTGAVIEFGGSVIRSLSEARMSCNM 234
DB 173 FKTMAYVDDRLPAGVTAKDIIILALIKIGTGGQGYVLEYRGSVIESMSMEGRMTICNM 232
QY 235 SIEGAGAGVAVPDEITFEYLKGRPLAPKYDSPMHKATQYKMLQSDPGAKYDIDVFID 294
DB 233 SIEAGARAAGVAVPDEITYEFLRDRPHAP--TGKQMDAAVAVWQQLRTDDDAVFDETVYLD 290
QY 295 AKDIVPTLTVGTSPEDEVVPIITGVVPDEPTEATEAKADGRRMLQYMGLIKAGTPEMEDI 354
DB 291 ATSLSPFVTWGTNPGQVPLAASVPDELMIDVARDQAERKALAYMDLRPSTPMRDIAVD 350
QY 355 KVFISGCTNSRIEDLRAAAANVKRKKAPNYSAMVPGSGLVTKQAEELDKIFEENAG 414
DB 351 AVFVGSCTNGRIEDLRVADVLRGHKVADGVR-WLIVPGSMRVRAQAEAGLGELFITAG 409
QY 415 FEMREAGCSMCLGNPDILAFQERCASTSNRNFEGROGAGGRTHLMSFVMAAAGIVG 472
DB 410 AQNRQPGCSMCLGNPDQLAFGERCAATSNRNFEGROGKGRTHLVSPAVAAATAVRG 467

Search completed: March 17, 2003, 08:50:42
Job time : 32 secs

